



1600

#11

RAW SEQUENCE LISTING

DATE: 09/23/2004

PATENT APPLICATION: US/09/331,127

TIME: 12:50:57

Input Set : A:\16777344.app

Output Set: N:\CRF4\09232004\I331127.raw

3 <110> APPLICANT: MUNROE, DONALD G.
 4 GUPTA, ASHWANI K.
 5 VYAS, TEJAL B.
 6 MCCALLUM, KIRK
 7 FAN, ERMI
 9 <120> TITLE OF INVENTION: CLONED GLUCAGON-LIKE PEPTIDE-2 RECEPTORS
 11 <130> FILE REFERENCE: 016777-0344
 13 <140> CURRENT APPLICATION NUMBER: 09/331,127
 14 <141> CURRENT FILING DATE: 1999-10-19
 16 <150> PRIOR APPLICATION NUMBER: PCT/CA97/00969
 17 <151> PRIOR FILING DATE: 1997-12-15
 19 <150> PRIOR APPLICATION NUMBER: 08/845,546
 20 <151> PRIOR FILING DATE: 1997-04-24
 22 <150> PRIOR APPLICATION NUMBER: 08/787,721
 23 <151> PRIOR FILING DATE: 1997-01-24
 25 <150> PRIOR APPLICATION NUMBER: 08/767,224
 26 <151> PRIOR FILING DATE: 1996-12-13
 28 <160> NUMBER OF SEQ ID NOS: 28
 30 <170> SOFTWARE: PatentIn Ver. 3.2
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 2575
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Rattus norvegicus
 37 <400> SEQUENCE: 1
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 39 gcaggaggcc accgcctgca gtacatcttg gagtggtgga gggatgtgcc tgcacttggtg 120
 40 aacgggcgcc aggagaatga ggcccccaacc aagcccggca gtgcccagta gatgcagaga 180
 41 ggcacccgtg ccccgagtga gggcacagcc agtgggcatc cctgaggccc aggggcccgt 240
 42 tcctctccac tcccaacaga tgcgtctgct gtggggccct gggaggccct tcctcgccct 300
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 44 gtgggctaata tataaggaga agtggtctgga agacttgac aatagacttt ctggcatatt 420
 45 ttgtaattggg acatttgatc ggtatgtgtg ctggcctcat tcttatcctg gaaatgtctc 480
 46 tgttccctgt ccttcatact taccttggtg gaatgcagag agcccaggaa gggcctacag 540
 47 acactgcttg gctcagggga cttggcagac gcgagagaac accacagata tttggcagga 600
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 53 gacatccgtc tctgtctgct ccgtccaggt cctcctgcac tactttgtgg gcaccaatca 960
 54 cttgtggctg ctgggtgaag gactttacct ccacactctg ctggagccca cagtgtttcc 1020
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 56 tattccctgg ggttttgccc gtgcacacct ggagaacaca cgggtgctggg ccacaaatgg 1140

(ps.6)

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57 gaacctgaaa atctggtgga tcatcagagg acccatgctg ctttgtgtaa cagttaattt 1200
58 cttcatcttc ctcaagattc tcaagcttct catttctaag ctcaaagctc atcagatgtg 1260
59 cttcagagac tacaaataca gattggcgaa atcaacgttg ctctcattc ctttgttggg 1320
60 ggttcatgag gtcctcttca ctttcttccc cgacgaccaa gttcaaggat tttcaaaacg 1380
61 tattcgactc ttcattccagc tgacactgag ctctgtccac ggatttctgg tggccttgca 1440
62 gtatggcttt gccaatggag aggtgaaggc agagctgcga aagtcatggg gccgcttctt 1500
63 attagccgcg cactggggct gcagaacctg tgtcctgggg aagaatttcc ggctcctggg 1560
64 gaagtgttcc aagaagctgt cggagggaga tggctctgag acactccaga agctgcgggt 1620
65 ctccacatgc agctcacacc tggcctctga gaccctggga gacgttgggg tacagcctca 1680
66 caggggccgt ggagcttggc cccggggaag cagcctgtct gagagcagtg agggagactt 1740
67 caccctggcc aatacgatgg aggagattct ggaagagagt gagatctaag gcagggtcca 1800
68 tcaccgcagc ttggccactg argamccaac cctargaagg atkttgccga rcccarggtc 1860
69 ctctcttctc tatgtwctat mcccattttg atgtgaagtc tctcctgggt gamcaasctc 1920
70 tgtaccaacs artctcagtc cctcttgccc ttgtcaccct actaccctc ccccatcaca 1980
71 catgttttcc agaatkccg ttggtttggg ggggggggtc ttgccctaaa ttcaagtsa 2040
72 gtggarccca ccatgaagaa aartcattta ttaaatarag tccggttagg atctccttcc 2100
73 cgttcatggt gcatggcctc cttccaaggg atgggagtcg gstgcactgg aacccacag 2160
74 gaaactttga agtatccagt tctagggaaat tatagccaat attctgagag agcaagtctg 2220
75 agatgagakc cgagaatwgc aagtgtwggg cawgcattca aggaaactcc tcacctttgg 2280
76 gcgaaaccta tggcaggatc ggcattggagc agctattmtg caayggccgc tcacctggga 2340
77 cataccactc tccttgggca ggatgtgacc ccatgtkgtc cccagactc ctctcctcct 2400
78 tgcttststt cytttccygt caagtctcac ctccctttct acatctcagt tcwgtttggg 2460
79 gtygacagaa gyytgaatgt cacaatactg catgtgttag tttctgtcgt cattgctgtg 2520
80 tccaaatacc tgaccaggac caatttaagc gaggaactgc tacatgggcg gccgc 2575

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83 <210> SEQ ID NO: 2

84 <211> LENGTH: 550

85 <212> TYPE: PRT

86 <213> ORGANISM: Rattus norvegicus

88 <400> SEQUENCE: 2

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89 Met Arg Pro Gln Pro Ser Pro Ala Val Pro Ser Arg Cys Arg Glu Ala
90 1 5 10 15
92 Pro Val Pro Arg Val Arg Ala Gln Pro Val Gly Ile Pro Glu Ala Gln
93 20 25 30
95 Gly Pro Val Pro Leu His Ser Gln Gln Met Arg Leu Leu Trp Gly Pro
96 35 40 45
98 Gly Arg Pro Phe Leu Ala Leu Leu Leu Val Ser Ile Lys Gln Val
99 50 55 60
101 Thr Gly Ser Leu Leu Lys Glu Thr Thr Gln Lys Trp Ala Asn Tyr Lys
102 65 70 75 80
104 Glu Lys Cys Leu Glu Asp Leu His Asn Arg Leu Ser Gly Ile Phe Cys
105 85 90 95
107 Asn Gly Thr Phe Asp Arg Tyr Val Cys Trp Pro His Ser Tyr Pro Gly
108 100 105 110
110 Asn Val Ser Val Pro Cys Pro Ser Tyr Leu Pro Trp Trp Asn Ala Glu
111 115 120 125
113 Ser Pro Gly Arg Ala Tyr Arg His Cys Leu Ala Gln Gly Thr Trp Gln
114 130 135 140
116 Thr Arg Glu Asn Thr Thr Asp Ile Trp Gln Asp Glu Ser Glu Cys Ser
117 145 150 155 160

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119 Glu Asn His Ser Phe Arg Gln Asn Val Asp His Tyr Ala Leu Leu Tyr
120                               165                               170                               175
122 Thr Leu Gln Leu Met Tyr Thr Val Gly Tyr Ser Val Ser Leu Ile Ser
123                               180                               185                               190
125 Leu Phe Leu Ala Leu Thr Leu Phe Leu Phe Leu Arg Lys Leu His Cys
126                               195                               200                               205
128 Thr Arg Asn Tyr Ile His Met Asn Leu Phe Ala Ser Phe Ile Leu Lys
129                               210                               215                               220
131 Val Leu Ala Val Leu Val Lys Asp Met Val Ser His Asn Ser Tyr Ser
132 225                               230                               235                               240
134 Lys Arg Pro Asp Asp Glu Ser Gly Trp Met Ser Tyr Leu Ser Glu Thr
135                               245                               250                               255
137 Ser Val Ser Cys Arg Ser Val Gln Val Leu Leu His Tyr Phe Val Gly
138                               260                               265                               270
140 Thr Asn His Leu Trp Leu Leu Val Glu Gly Leu Tyr Leu His Thr Leu
141                               275                               280                               285
143 Leu Glu Pro Thr Val Phe Pro Glu Arg Arg Leu Trp Pro Lys Tyr Leu
144                               290                               295                               300
146 Val Val Gly Trp Ala Phe Pro Met Leu Phe Val Ile Pro Trp Gly Phe
147 305                               310                               315                               320
149 Ala Arg Ala His Leu Glu Asn Thr Arg Cys Trp Ala Thr Asn Gly Asn
150                               325                               330                               335
152 Leu Lys Ile Trp Trp Ile Ile Arg Gly Pro Met Leu Leu Cys Val Thr
153                               340                               345                               350
155 Val Asn Phe Phe Ile Phe Leu Lys Ile Leu Lys Leu Leu Ile Ser Lys
156                               355                               360                               365
158 Leu Lys Ala His Gln Met Cys Phe Arg Asp Tyr Lys Tyr Arg Leu Ala
159                               370                               375                               380
161 Lys Ser Thr Leu Leu Leu Ile Pro Leu Leu Gly Val His Glu Val Leu
162 385                               390                               395                               400
164 Phe Thr Phe Phe Pro Asp Asp Gln Val Gln Gly Phe Ser Lys Arg Ile
165                               405                               410                               415
167 Arg Leu Phe Ile Gln Leu Thr Leu Ser Ser Val His Gly Phe Leu Val
168                               420                               425                               430
170 Ala Leu Gln Tyr Gly Phe Ala Asn Gly Glu Val Lys Ala Glu Leu Arg
171                               435                               440                               445
173 Lys Ser Trp Gly Arg Phe Leu Leu Ala Arg His Trp Gly Cys Arg Thr
174                               450                               455                               460
176 Cys Val Leu Gly Lys Asn Phe Arg Phe Leu Gly Lys Cys Ser Lys Lys
177 465                               470                               475                               480
179 Leu Ser Glu Gly Asp Gly Ser Glu Thr Leu Gln Lys Leu Arg Phe Ser
180                               485                               490                               495
182 Thr Cys Ser Ser His Leu Ala Ser Glu Thr Leu Gly Asp Val Gly Val
183                               500                               505                               510
185 Gln Pro His Arg Gly Arg Gly Ala Trp Pro Arg Gly Ser Ser Leu Ser
186                               515                               520                               525
188 Glu Ser Ser Glu Gly Asp Phe Thr Leu Ala Asn Thr Met Glu Glu Ile
189                               530                               535                               540
191 Leu Glu Glu Ser Glu Ile

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Input Set : A:\16777344.app

Output Set: N:\CRF4\09232004\I331127.raw

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192 545                               550
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196 <211> LENGTH: 33
197 <212> TYPE: DNA
198 <213> ORGANISM: Artificial Sequence
200 <220> FEATURE:
201 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
202     primer
204 <220> FEATURE:
205 <221> NAME/KEY: modified_base
206 <222> LOCATION: (24)
207 <223> OTHER INFORMATION: a, c, g, t, unknown, or other
209 <400> SEQUENCE: 3
W--> 210 tttttctaga asrtsatsta cacngtsggc tac                               33
213 <210> SEQ ID NO: 4
214 <211> LENGTH: 32
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
220     primer
222 <400> SEQUENCE: 4
223 ttttctcgag ccarcarcca sswrtarttg gc                               32
226 <210> SEQ ID NO: 5
227 <211> LENGTH: 38
228 <212> TYPE: DNA
229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
233     oligonucleotide
235 <400> SEQUENCE: 5
236 aactacatcc acmkgmayct gttvygtcb ttcatsct                               38
239 <210> SEQ ID NO: 6
240 <211> LENGTH: 25
241 <212> TYPE: DNA
242 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
245 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
246     primer
248 <400> SEQUENCE: 6
249 tcatctccct cttcttggt cttac                                           25
252 <210> SEQ ID NO: 7
253 <211> LENGTH: 25
254 <212> TYPE: DNA
255 <213> ORGANISM: Artificial Sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
259     primer
261 <400> SEQUENCE: 7

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RAW SEQUENCE LISTING

DATE: 09/23/2004

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Input Set : A:\16777344.app

Output Set: N:\CRF4\09232004\I331127.raw

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262 tctgacagat atgacatcca tccac 25
265 <210> SEQ ID NO: 8
266 <211> LENGTH: 32
267 <212> TYPE: DNA
268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
272 primer
274 <220> FEATURE:
275 <221> NAME/KEY: modified_base
276 <222> LOCATION: (5)
277 <223> OTHER INFORMATION: a, c, g, t, unknown, or other
279 <400> SEQUENCE: 8
W--> 280 tcyrnctgsa cctcmmyrrtt gasraarcag ta 32
283 <210> SEQ ID NO: 9
284 <211> LENGTH: 667
285 <212> TYPE: DNA
286 <213> ORGANISM: Homo sapiens
288 <220> FEATURE:
289 <221> NAME/KEY: CDS
290 <222> LOCATION: (1)..(666)
292 <400> SEQUENCE: 9
293 tcc ttc tct ctt atc tcc ctc ttc ctg gct ctc acc ctc ctc ttg ttt 48
294 Ser Phe Ser Leu Ile Ser Leu Phe Leu Ala Leu Thr Leu Leu Leu Phe
295 1 5 10 15
297 ctt cga aaa ctc cac tgc acg cgc aac tac atc cac atg aac ttg ttt 96
298 Leu Arg Lys Leu His Cys Thr Arg Asn Tyr Ile His Met Asn Leu Phe
299 20 25 30
301 gct tct ttc atc ctg aga acc ctg gct gta ctg gtg aag gac gtc gtc 144
302 Ala Ser Phe Ile Leu Arg Thr Leu Ala Val Leu Val Lys Asp Val Val
303 35 40 45
305 ttc tac aac tct tac tcc aag agg cct gac aat gag aat ggg tgg atg 192
306 Phe Tyr Asn Ser Tyr Ser Lys Arg Pro Asp Asn Glu Asn Gly Trp Met
307 50 55 60
309 tcc tac ctg tca gag atg tcc acc tcc tgc cgc tca gtc cag gtt ctc 240
310 Ser Tyr Leu Ser Glu Met Ser Thr Ser Cys Arg Ser Val Gln Val Leu
311 65 70 75 80
313 ttg cat tac ttt gtg ggt gcc aat tac tta tgg ctg ctg gtt gaa ggc 288
314 Leu His Tyr Phe Val Gly Ala Asn Tyr Leu Trp Leu Leu Val Glu Gly
315 85 90 95
317 ctc tac ctc cac acg ctg ctg gag ccc aca gtg ctt cct gag agg cgg 336
318 Leu Tyr Leu His Thr Leu Leu Glu Pro Thr Val Leu Pro Glu Arg Arg
319 100 105 110
321 ctg tgg ccc ara tac ctg ctg ttg ggt tgg gcc ttc cct gtg cta ttt 384
W--> 322 Leu Trp Pro Xaa Tyr Leu Leu Leu Gly Trp Ala Phe Pro Val Leu Phe
323 115 120 125
325 gtt gta ccc tgg ggt ttc gcc cgt gca cac ctg gar aac aca ggg tgc 432
326 Val Val Pro Trp Gly Phe Ala Arg Ala His Leu Glu Asn Thr Gly Cys
327 130 135 140

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/331,127

DATE: 09/23/2004
TIME: 12:50:58

Input Set : A:\16777344.app
Output Set: N:\CRF4\09232004\I331127.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 24
Seq#:8; N Pos. 5
Seq#:9; Xaa Pos. 116
Seq#:10; Xaa Pos. 116

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/331,127

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Input Set : A:\16777344.app

Output Set: N:\CRF4\09232004\I331127.raw

L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:322 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:9
L:322 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:384
L:382 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:112